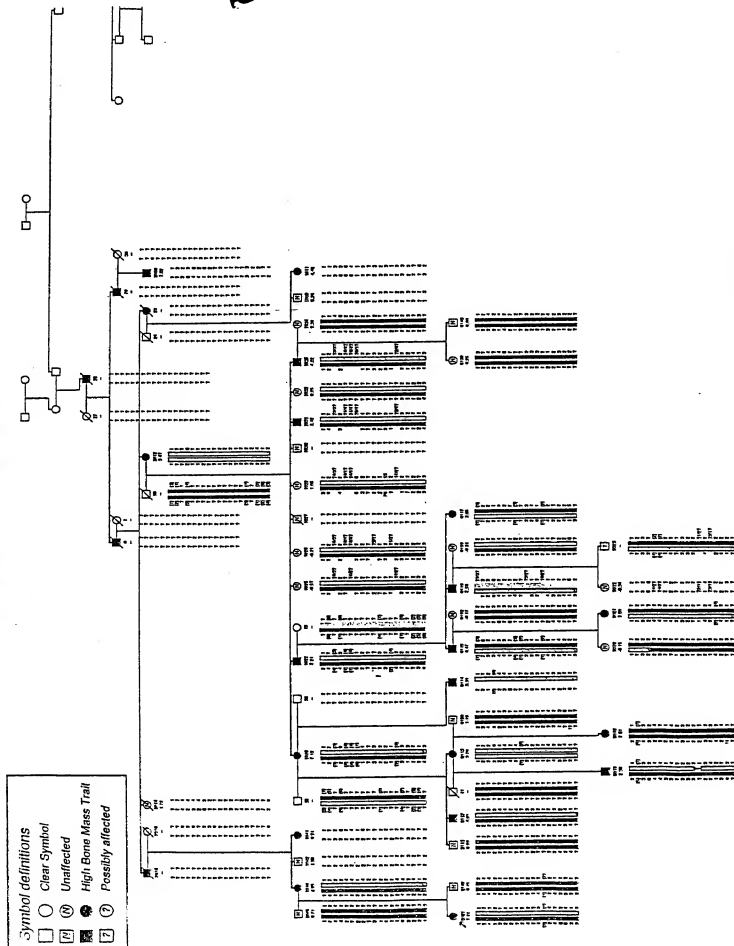
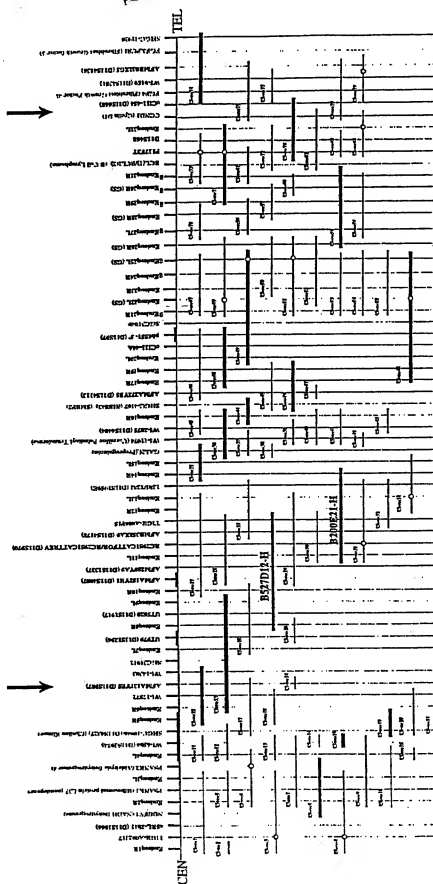


Figure 1.
EBM haplotype indicated with crosshatch



EST/Clone
Anonymous STS
STSs from BAC Ends
Genetic Marker

BAC/STS Map of the HBM Region



— BAC - HTS Complete

— Homology on other chromosomes

Exon 1

ACTAAAGCGCCGCCGCCGCCATGGAGCCCGAGTGAGCGCGGCGCGG
GCCCGTCCGGCCGCCGGACAACATGGAGGCAGCGCCGCCGGCCGCCG
GTGGCCCGTGTCTGTCTGTCTGTCTGTGGCGCTGTGCGGCTGC
CCGGCCCCCGCCGCCGCC

Exon 2 Coordinates: 527d12_Contig308G 30944-30549

gccccacagCCTCGCGCTCCTGCTATTTGCCAACCGCCGGGACGTACGGCTG
GTGGACGCGCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCC
TGGAGGATGCGGCCGCGAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTA
CTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAG
ACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCG
ACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTA CTGGACGGACTC
AGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAG
GTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGCCTTGGACC
CCGCTCACGGgttaacctgctg

... 9408 nt ...

Exon 3 Coordinates: 527d12_Contig308G 21141-20945

ccccgtcacagGTACATGTA CTGGACAGACTGGG GTGAGACGCCCCGGATTGA
GCGGGCAGGGATGGATGGCAGCACCCCGGAAGATCATTGTGGACTCGGAC
ATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCT
ACTGGGCTGACGCCAAGCTCAGCTTCATCCACCCGTGCCAACCTGGACGG
CTCGTTCCGgtgagtaccac

... 6094 nt ...

Exon 4 Coordinates: 527d12_Contig308G 15047-14850

tcctgactgcagGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCC
TGACGCTCTCCGGGGACACTCTGTA CTGGACAGACTGGCAGACCCGCTC
CATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTG
AGTGCCCTATACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGCG
AGCCTTTCTgtgagtgccg

... 1827 nt ...

Exon 5 Coordinates: 527d12_Contig308G 13220-13088

tttctcagTCCACATCGCTGTGAGGAGGACAATGGCGGGTGTCTCCACCTGT
GCCTGTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCACACGGG
TGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGgtgaggcggaggagc

FIGURE 3A

... 20923 nt ...

Exon 6 Coordinates: 527d12_Contig309G 7705-8100

ctccacagGAGCCGAGGAGGTGCTGCTGCTGGCCCGGGCGGACGGACCTACGG
AGGATCTCGCTGGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGG
ACGACATCCGGGACGCCATTGCCATCGACTACGACCCGCTAGAGGGCTA
TGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGACAGGGCGTACCTG
GACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGACCCCG
ATGGCATCGCGGTGCGACTGGGTGGCCCGAAACCTCTACTGGACCGACAC
GGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAG
ATCCTGGTGTGCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACC
CCGTGATGGGgtaagacgggc

..... 3211 nt

Exon 7 Coordinates: 527d12_Contig309G 11311-11482

ttctctccagCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAAATCGAGT
GTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCT
CGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTAC
TGGGGAGACGCCAAGACAGACAAGATCGAGgtgaggtcctctgtgg

..... 13445 nt

Exon 8 Coordinates: 527d12_Contig309G 24927-25143

ccgtcctcgagGTGATCAATGTTGATGGGACGAAGAGGGCGGACCCTCCTGGAG
GACAAGCTCCCGCACATTTTCGGGTTTCACGCTGCTGGGGGACTTCATCTA
CTGGACTGACTGGCAGCGCCGCGAGCATCGAGCGGGTGCACAAGGTCAAG
GCCAGCCGGGACGTGCATCATTGACCAGCTGCCCGACCTGATGGGGCTCA
AAGCTGTGAATGTGGCCAAGGTCTGTCGgtgagtcgggggggtc

....2826 nt

Exon 9 Coordinates: 527d12_Contig309G 27969-28256

gttcgctccagGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGACGCCACC
TGTGCTTCTTACACCCACGCAACCCGGTGTGGCTGCCCCATCGGCCT
GGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTG
GTCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATA
ACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCT
GGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTGAGCCTGA
AGgtagcgtgggc

.....3102.....

FIGURE 3B

Exon 10 Coordinates: 527d12_Contig309G 31358-31582

cctgctgccagACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCAC
GTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGA
TGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGT
GGCGCGGCTGGACGGGCAGTTCGGCAAGTCCTCGTGTGGAGGGACTTG
GACAACCCGAGGTCGCTGGCCCTGGATCCCCACCAAGGGGtaagtgttgcctgtc

.....1297 nt.....

Exon 11 Coordinates: 527d12_Contig309G 32879-33064

gtgcctccagCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTG
CGGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGG
GCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCGCCTCTACTG
GACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGgtgagggcc
gggct

.....2069 nt.....

Exon 12 Coordinates: 527d12_Contig309G 35133-35454

gtgttcacgagGTGAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCGT
TCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTG
CACAGCATTGAGCGGGCCGACAAGACTAGCGGGCCGGAACCGCACCCCTCA
TCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCACCTCCTCC
CGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGC
AGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACA
CTACACCCTGGACCCAGCAGCCGCAACTGCAGCCgtaagtgcctcatgtt

.....2006 nt.....

Exon 13 Coordinates: 527d12_Contig309G 37460-37659

gcctcctctaCGCCACACCTTCTTGCTGTTGAGCCAGAAATCTGCCATCAGT
CGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCTGCCCTGC
ATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTT
CATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGAC
GGGACCCAGgcagggtgcctgtgg

.....6965 nt.....

FIGURE 3C

Exon 14 Coordinates: 527d12_Contig309G 44624-44832

cttgttcttaccagCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACA
GGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTG
GACGTGCGAGGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAA
GCCATGGGGGTGGTGGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATC
GTCGTCAACGCGGAGCGAGGgttaggaggccaac

.....1404 nt.....

Exon 15 Coordinates: 527d12_Contig309G 46236-46427

ccaccctcccagGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGA
TCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCTCTTCAACCAC
CGGCCTCATCCGCCCTGTGGCCCTGGTGGTGGAACAACACTGGGCAAG
CTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGT
CAGgtacgcgccccgg

.....686 nt.....

Exon 16 Coordinates: 527d12_Contig309G 47113-47322

ggctgcttcagGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGACG
CTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCA
GCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACT
CGCATCCAGGGCCGTGTCGCCACCTCACTGGCATCCATGCAGTGGAGG
AAGTCAGCCTGGAGGAGTTCTgtacgtgggggc

.....3884 nt.....

Exon 17 Coordinates: 527d12_Contig309G 51206-51331

ttgttcttcagCAGCCCACCATGTGCCCCTGACAATGGTGGCTGCTCCACAT
CTGTATTGCCAAGGGTGATGGGACACCAGGTGCTCATGCCAGTCCAC
CTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGgttaggtgtgacctaggtgc

....3905 nt.....

Exon 18 Coordinates: 527d12_Contig309G 55236-55472

gttctctctgtccctccccagAGCCGCCCCACCTGCTCCCCGGACCAGTTTGCATGTGC
CACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTT
CCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCGTGTGCTCCG
CCGCCAGTTCCCTTGCAGCGCGGGGTCACTGTGTGACCTGCGCCTGCG
CTGCGACGCGGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGT
GACGgtgaggccctcc

.....3052 nt.....

FIGURE 3D

00572000.125640

Exon 19 Coordinates: 527d12_Contig309G 58524-58634

tctcttgccagCCATCTGCCTGCCCAACCA GTTCCGGTGTGCGAGCGGCCAGTG
TGTCCTCATCAAACAGCAGTGC GACTCCTTCCCCGACTGTATCGACGGCT
CCGACGAGCTCATGTGTGgtgagccagctt

.....1448 nt.....

Exon 20 Coordinates: 527d12_Contig309G 60082-60319

gtttgtctctggcagAAATCACCAAGCCGCCCTCAGACGACAGCCCCGGCCCCACAGC
AGTGCCATCGGGCCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGG
TGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGG
GCCAACGGGGCCCTTCCCCGACGAGTATGTACGCGGGGACCCCGCACGTGC
CCCTCAATTTTCATAGCCCCGGGCGGTTCCAGCATGGCCCTTCACAGgta
aggagcctgagatatggaa

....1095 nt.....

Exon 21 Coordinates: 527d12_Contig309G 61414-61552

cttccttgccagGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGA
TGGGGGGCCGGGGCGGGGTGCCCTCTACGACCGGAACCACGTACAG
GGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGTGTACCCGCC
Ggtgagggcgggg

.....6513 nt.....

Exon 22 Coordinates: 527d12_Contig309G 68065-68162

ttggctctctcagATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTG
TACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACC
GTACAGtaggacatccccgcag

.....2273 nt.....

FIGURE 3E

Exon 23 Coordinates: 527d12_Contig309G 70435-70901

tcaaacattccggccactgcgagaccgtacagGCCCTACATCATTTCGAGGAATGGCGCCCCC
GACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGC
CGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACC
CCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTGGCGGGAGGA
CAGCTGCCCCGCCCTCGCCCCGCCACCGAGAGGAGCTACTTCCATCTCTTC
CCGCCCCCTCCGTCCCCCTGCACGGACTCATCTGACCTCGGCCGGGCCA
CTCTGGCTTCTCTGTGCCCCCTGTAAATAGTTTTAAATATGAACAAAGAAAAA
ATATATTTATGATTAAAAAATAAATATAATTGGGATTTAAAAACATGAGA
AATGTGAAGTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGGAG
AAATATTTATAAACTTAATTTTGTAACA

FIGURE 3F

Figure 4

Model for a LDL Receptor-Related protein, Zmax1

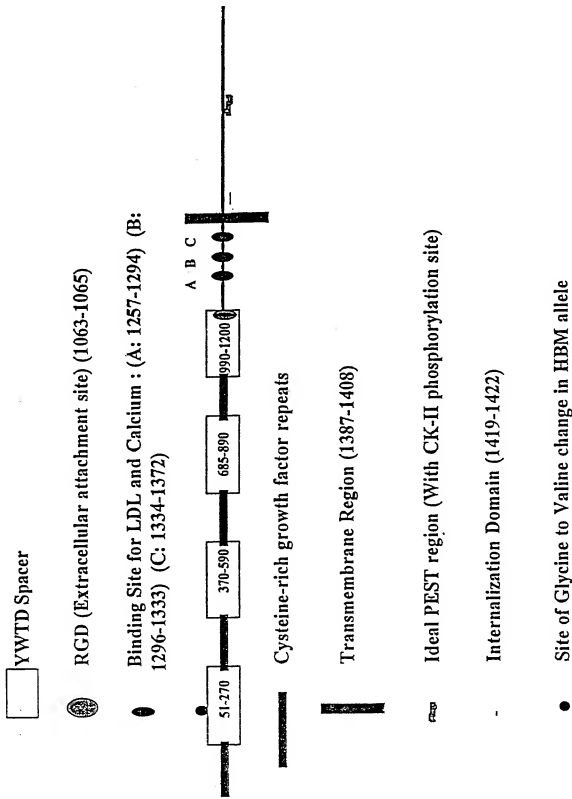
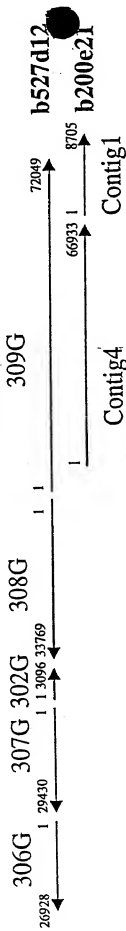
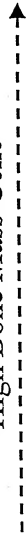


Figure 5

High Bone Mass Gene



1	ACTAAAGCGCGCGCGCGCGCCATGGAGCCCGAGTGAGCGCGCGCGCGCGCGCGCTCCGGCC	60
61	GCCGGACAACATCGGAAGGACCGCGCGCGCGCGCGCGCTGTGCTGTCTGCTGTCTGCT	120
1	M E A A A P P G P P L L L L L L L L	17
121	GCTGCTGCTGCGCGCTGTGCGGCTGCCCGSCCCCCCGCGGGCCTCGCGCTCTGTGTTATT	180
18	L L L L A L C G C P A P A A A S P L L L L F	37
181	TGCCAACCGCGGGACGTACGGCTGGTGAGCGCGCGCGGATCAAGLCTGGAGCTCCACCAT	240
38	A N R R C R G L V D A G G V K L E S T I	57
241	CGTGCTCAGCGGCTGGAGGATCGCGCGCGAGTGGACTTCCAGTTTTCGAAGGGAGCCCT	300
58	V V S G L E D A C A V D F Q F S K G A V	77
301	GTACTGGACAGCTGACGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC	360
78	Y W T D V S E E A I K Q T Y L N Q T G A	97
361	CGCGCTCAGAAACGTGTCCTCCGGCTGGTCTCTCCGACGGCTCGCTCGCGACTG	420
98	A V G N V V I S G L V S P D G G L A C D W	117
421	GGTGGGCAAGAAGCTGTACTGGACGGAATCAGAGACCAACCGCATCGAGGTGGCCAACT	480
118	V G K K L L Y W T D T T S E T N R I E V A N L	137
481	CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCCGAGGGCGCTCGC	540
138	N G T S R K A V L F W Q D L Q P R A I A	157
541	CTTGGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA	600
158	L D P F A H G Y M Y W T D W G E T P R I E	177
601	CGGCGCAGGATGGATTGGCAGCACCCGGAAGATCAITGTGACTCGGACATTACTGGCC	660
178	A G M D G S T R K A I I V D G S D I Y W P	197
661	CAATGGACTACCATCGACTCGGAGGACGAAAGCTCTACTGGGCTGACGCCAAGCTCAG	720
198	N G L T T I D L E E Q K L Y W A D A K L S	217
721	CTTACTCCACCTGCCAACCTGGACTCGTTCGCGCAGAAGGTGGTGGAGGGCAGCCT	780
218	F I H R A N L D G S F R C T G V V E A G S L	237
781	GACGCAACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC	840
238	T H P F A L T L S G D T L Y W T D W Q T	257
841	CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC	900
258	R S I H A C N K R T G G K R K E I L S A	277
901	CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGCAGCCTTTCTCCACAC	960
278	L Y S P M D I Q V L S Q E R Q P F F H T	297
961	TCGCTGTGAGGAGACATGGCGGCTGCTCCCACTGTGCTGCTGTCCCCAAGSGAGCC	1020
298	R C E E D N G A C S H L C L S L S P G E	317
1021	TTTCTACACATGCGCGCTGCCACCGGGTGTGCGACTGTCAGGACAACGGCAGGACGTGTAA	1080
318	F Y T C A C P T G V Q L Q D N G R T C K	337
1081	GGCAGGAGCCGAGGAGTGTCTGTCTGACCCCGCGGACCTACGGAGGATCTCGCT	1140
338	A G A E E V L L L L L R R T D L R R I S L	357

Figure 6A

1141 GGACACGCCGACTTACCACGACATCGTGCTGCAGGTGGACGACATCCGGCAGGCCATTGC 1200
358 D T P D F T D I V L Q V D D I R H A I A 377

1201 CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT 1280
378 I D Y D P L E G Y V Y W T D D E V R A I 397

1261 CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA 1320
398 R R A Y L D G S G A Q T L V N T E I N D 417

1321 CCCCAGATGGCATCGCGGTGACTGGGTGGCCCCGAAACCTCTACTGGACCGACACGGGCAC 1380
418 P D G I A V D W V A R N L Y W T D T G T 437

1381 GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGAAGATCCTGGTGTGCGGAGGA 1440
438 D R I E V T R L N G T S R K I L V S E D 457

1441 CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGCCCTCATGTACTGGACAGA 1500
458 L D E P R A I A L H P V M G L M Y W T D 477

1501 CTGGGGAGAGAACCTTAAATCGAGTGTGCCAAGTGGATGGGCAGGAGCGCGTGTGCT 1560
478 R G E N P K I E C A N L D G Q E R R V L 497

1561 GGTCAATGCTCCCTCGGGTGGCCCAACGCGCTGGCCCTGGACCTGCAGGAGGGGAAGCT 1620
498 V N A S L G W F P N G L A L D L Q E G K L 517

1621 CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG 1680
518 Y W G D A K T D K I E V I N V D G T K R 537

1681 GCGGACCTCTGGGAGGACAAGCTCCCGCACATTTTCGGGTTTCAGCTGCTGGGGGACTT 1740
538 R T L L E D K L P H I F G F T L L G D F 557

1741 CATCTACTGGACTGACTGGCAGCGCCGACGATCGAGCGGGTGACACAAGGTCAAGGCCAG 1800
558 I Y W T D W Q R R S I E R V H K V K A S 577

1801 CCGGGACGTCATCATTGACAGCTGCCCCAGCTGATGGGGCTCAAAGCTGTGAATGTGGC 1860
578 R D V I I D Q L P D L M G L K A V N V A 597

1861 CAAGGTGCTCGGAACCAACCCGCTGTGCGGACAGGAACGGGGGTGCAGCCACCTGTGCTT 1920
598 K V V G T N P C A D R N G G C S H L C F 617

1921 CTTACACCCCGCAACCCCGGTGTGGCTGCCCATCGGCCTGGAGCTGTGTAGTGACAT 1980
618 F T P H A T R C G C P I G L E L C D M 637

1981 GAAGACCTGCATGCTGCTGAGGCCTTCTGGTCTTCACCAGCAGAGCCGCCATCCACAG 2040
638 K T C I V P E A F L V F T S R A A I H R 657

2041 GATCTCCCTCGAGCCAATAACAACGACGTGGCCATCCCGCTCACGGCGTCAAGGAGGC 2100
658 I T S L E T N N N D V A I P L T G V K E A 677

2101 CTCAGCCCTGGACTTTGATGTGTCCAACAACCATCTACTGGACAGACGTGAGCCTGAA 2160
678 S A L D F D V S N N H I Y W T D V S L K 697

2161 GACCATCAGCCCGCCTTCATGAACGGGAGCTCGGTGGAGCACGCTGGTGGAGTTTGGCCT 2220
698 T I S R A F M N G S S V E H V V E F G L 717

Figure 6B

2221	TGACTACCCCCAGGGCATGGCCGTTGACTGGATGGGCAAGAACCCTCTACTGGGGCGGACAC	2230
718	D Y P E G M A V D W M G K N L Y W A D T	737
2281	TGGGACCAACAGAAATCGAAGTGGCGCGCTGGACGGGCGAGTTCGGGCAAGTCTCTGTTG	2340
738	G T N R I E V A R L D G Q F R Q V L V W	757
2341	GAGGGACTTGGACAACCCGAGGTCTGCTGGCCCTGGATCCCCACCAAGGGCTACATCTACTG	2400
758	R D L D N P R S L A L D P T K G Y I Y W	777
2401	GACCGAGTGGGGCGGCAAGCCGAGGATCTGCGGGGCTTCATGGACGGGACCAACTGCAT	2460
778	T E W G G K P R I V R A F M D G T N C M	797
2461	GACGCTGGTGGACAAGTGGGCGGGCCAAACGACCTCACCATTGACTACGCTGACCCAGCG	2520
798	T L V D K V G R A N D L T I D Y A D Q R	817
2521	CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCTGCTCAACATGCTGGGTACAGGA	2580
818	L Y W T D L D T N M I E S S N M L G Q E	837
2581	CGCGTCTGTGATTGCCGACGATCTCCCGCACCCGTTCTGCTCTGACGAGTACAGCGATTA	2640
838	R V V I A D D L P H P F G T Q Y S D Y	857
2641	TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAGACTAGCGGCCG	2700
858	I Y W T D W N L H S I E R A D K T S G R	877
2701	GAACCGCACCTTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTCCACTC	2760
878	N R T L I Q G H L D F V M D I L V F H S	897
2761	CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCGAGTGTGGGCGAGTGTG	2820
898	S R Q D G L N D C M H N N G Q C G Q L C	917
2821	CCTTCCATCCCCGGCGGCCACGCTGCGGGCTGCGCCTCACACTACACCTGGACCCCGAG	2880
918	L A I P G G H R C G G C A S H Y T L D P S	937
2881	CAGCCGCAACTGCAGCCCGCCCAACCTCTCTGCTGTTGAGCCAGAAATCTGCCATCAG	2940
938	S R N C S P P T T F L L F S Q K S A I S	957
2941	TCCGATGATCCCCGACGACAGCACAGCCCGGATCTCATCCTGCCCTGTCATGGACTGAG	3000
958	R M I P D D Q H S P D L I L P L H G L R	977
3001	GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGTGGATGGGCG	3060
978	N V K A I D Y D P L D K F I Y W V D G R	997
3061	CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTGGACCTCTCTGAG	3120
998	Q N I K R A K D D G T Q P F V L T S L S	1017
3121	CAAAGGCCAAACCCAGACAGGCGAGCCCCACGACCTCAGCATCTACAGCCGGAC	3180
1018	Q G Q N P R D R Q P H D L S I D I Y S R T	1037
3181	ACTGTTCTGGAGCTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC	3240
1038	L F W T C E A T N T I N V H R L S G E A	1057
3241	CATGGGGTGTGTGCTGCGTGGGGACCGGACAGCCAGGGCCATCGTCTCAACGCGGA	3300
1058	M G V V L R G D R D K P R A I V V N A E	1077

Figure 6C

3301 GCGAGGGTACCTGTACTTACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC 3360
1078 R G Y L Y F T N M Q D R A A K I E R A A 1097

3361 CCTGGACGGCACCAGCGCGAGGTCTCTTCAACACCGGCCTCATCCGCCCTGTGGCCCT 3420
1098 L D G T E R E V L F T T G L I R P V A L 1117

3421 GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA 3480
1118 V V D N T L G K L F W V D A D L K R I E 1137

3481 GAGCTGTGACCTGTGAGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGCC 3540
1138 S C D L S G A N R L T L E D A N I V Q P 1157

3541 TCTGGGCGTGAACCTCCTTGGCAAGCATCTCTACTGGATCGACCGCCGACGAGCAGATGAT 3600
1158 L G L T I L G K H L Y W I D R Q Q Q M I 1177

3601 CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTGCGCCA 3660
1178 E R V E K T T G D K R T R I Q G R V A H 1197

3661 CCTCACTGGCATCCATGCGATGGAGGAAGTCAGCCTGGAGGAGTTCTCAGGCCACCCATG 3720
1198 L T G I H A V E E V S L E E F S A H P C 1217

3721 TGCCCGTGCAATGGTGGCTGTCTCCACACATCTGTATTGCCAAGGGTATGGGACACACG 3780
1218 A R D N G G C S H I C I A K G D G T P R 1237

3781 GTGCTCATGCCAGTCACCTCGTGTCTCTGCAGAACCTGTGACCTGTGGAGAGCCGCC 3840
1238 C S C P V H L V L L Q N L L T C G E P P 1257

3841 CACCTGTCTCCCCGACCCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC 3900
1258 T C S P D Q F A C A T G E I D C I P G A 1277

3901 CTGGCGCTGTGACGGCTTTCGCCAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT 3960
1278 W R C D G F P E C D D Q S D E E G C P V 1297

3961 GTGCTCCGCCGCCAGTTCCCTGTGCGCGGGGGTCACTGTGTGGACCTGCGCCTGCGCTG 4020
1298 C S A A Q F P C A R G Q C V D L R L R C 1317

4021 CGACGGCGAGGCGAGCTGTCAAGGACCGCTCAGACGAGGTGGATGTGACGCCATCTGCGCT 4080
1318 D G E A D C Q D R S D E V D C D A I C L 1337

4081 GCCCAACCACTTCCGGTGTGCGAGCGGCCAGTGTGTCTCATCAACAGCAGTGGGACTC 4140
1338 P N Q F R C A S G Q C V L I K Q C D S 1357

4141 CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAATCACCAGCCGCCCTC 4200
1358 F P D C I D G S D E L M C E I T K P P S 1377

4201 AGACACAGCCCCGCCACAGCAGTGCCATCGGGCCCGTCATTGGCATTATCTCTCTCT 4260
1378 D D S P A H S S A I G P V I G I I L S L 1397

4261 CTTCTCATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG 4320
1398 F V M G G V Y F V C Q R V V C Q R Y A G 1417

4321 GGCCCAACGGGCCCTTCCCGCACGATGTGACGCGGACCCCGCAGTGCCTCAATT 4380
1418 A N G P F P H E Y V S G T P H V P L N F 1437

Figure 6D

4381	CATAGCCCCGGGCGGTTCCAGCATTGGCCCTTCACAGGCATCGCATCGCGAAAGTCCAT	4440
1438	I A P G G S Q H G P F T G I A C G K S M	1457
4441	GATGAGCTCCGTGA3CTGTATGGGGGGCCGGGGCGGGCTTACGACCGGAACCA	4500
1458	M S S V S L G M G G R G G V P L Y D R N H	1477
4501	CGTCACAGGGGCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCGGAT	4560
1478	V T G A A S S S S S S S S S T K A T L Y P P I	1497
4561	CCTGAACCCGCCCTCCCCGCCACCGACCCCTCCCTGTACAACATGGACATGTTCTA	4620
1498	L N P P P S P F A T D P S L Y N M D M F Y	1517
4621	CTCTTCAAACATTCCGGCCACTCGGAGACCGTACAGGCCCTACATCATTGAGGAATGGC	4680
1518	S S N I P A T A R R P Y R P Y I I R G M A	1537
4681	GCCCCGACGACGCCCTCGAGCACCAGCTGTGTGACAGCGACTACAGCGCCAGCCGCTG	4740
1538	P P T T P C S T D V C D S D Y S A S R W	1557
4741	GAAGGCCAGCAAGTACTACCTGGATTGAACCTCGGACTCAGACCCCTATCCACCCACC	4800
1558	K A S S K Y Y L L D L N S D S D P Y P P P P	1577
4801	CACGCCCCACAGCCAGTACCTGTCCGGCGGAGGACAGCTGCCCGCCCTGCCCGCCACCGA	4860
1578	T P H S Q Y L S A E D S C P P S P A T E	1597
4861	GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCTGACC	4920
1598	R S Y F H C T P P P S P C T D S S	1615
4921	TCGGCCGGGCGACTCTGGCTTCTCTTGCCCTGTAAATGCTTTTAAATATGAACAAGA	4980
4981	AAAAAATATATTTATGATTTAAAAAATAAATAAATGGGATTTTAAAAACATGAGAAA	5040
5041	TGTGAACCTGTGATGGGGTGGGCGAGGCTGGGAGAACTTTGTACAGTGGAGAAATTTAT	5100
5101	AAACTTAATTTTGTAAAAACA	5120

Figure 6E

Northern Blot Analysis - Zmax 1

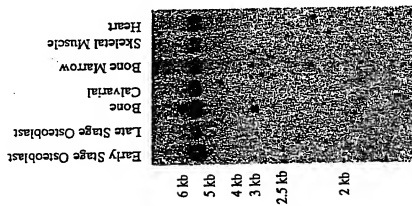


Figure 7B

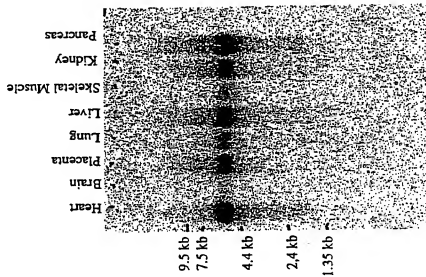
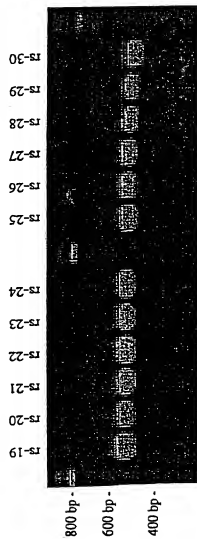


Figure 7A

Figure 8

Zmax 1 random samples

b527d12-h_Config087C_1.nt



00578000-002500

ASO Detection of the Zmax1 Exon 3 Mutation

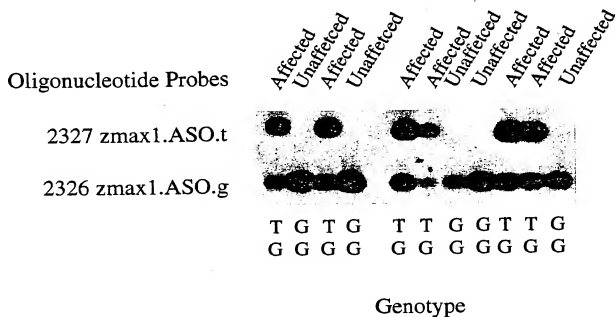
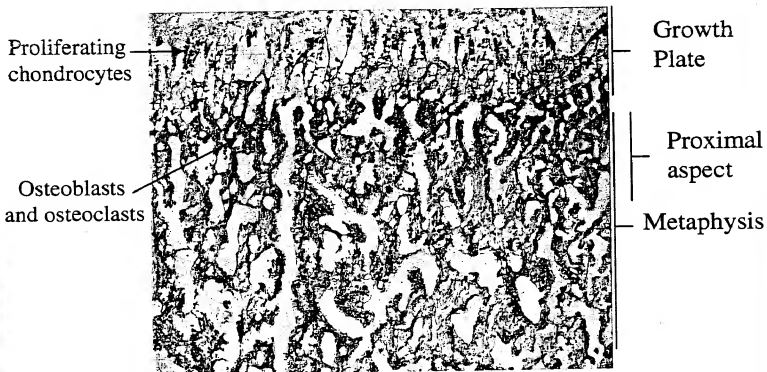


FIG. 9

Mouse Zmax1 In situ hybridization
100X Magnification

Antisense probe



Sense probe

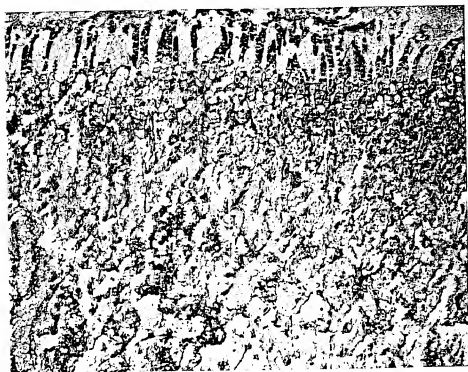


FIG. 10

009250-00687560

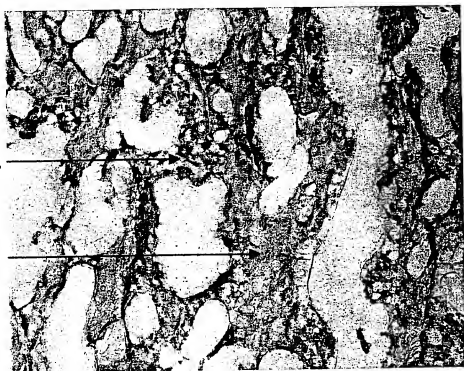
Mouse Zmax1 In situ hybridization
400X magnification

Antisense probe

Osteoblasts
and osteoclasts

Trabecular
bone

Proximal
Metaphysis



Sense probe



FIG. 11

09578900-052600

Mouse Zmax1 In situ hybridization
400X magnification

Antisense probe

Osteoblasts

Endosteum



Sense probe

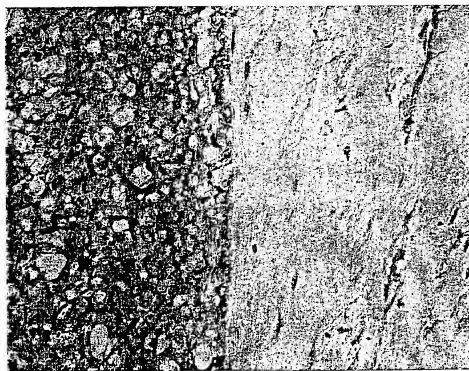
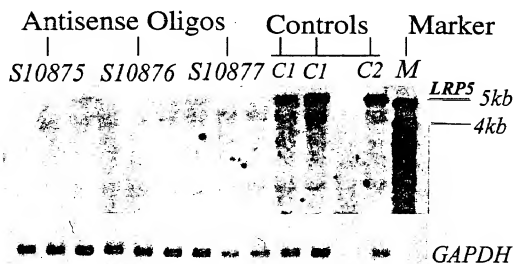


FIG. 12

Antisense Inhibition of Zmax1 Expression



MC-3T3 cells

FIG. 13